

0280



O I P E

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/047,253

DATE: 02/06/2002
 TIME: 19:09:22

Input Set : A:\CIT1510-4.ST25.txt
 Output Set: N:\CRF3\02062002\J047253.raw

ENTERED

2 <110> APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
 3 COPE, Gregory
 4 VERMA, Rati
 5 ARAVIND, L
 6 KOONIN, Eugene
 7 DESHAIES, Raymond
 9 <120> TITLE OF INVENTION: REGULATION OF TARGET PROTEIN ACTIVITY THROUGH MODIFIER

PROTEINS

11 <130> FILE REFERENCE: CIT1510-4
 13 <140> CURRENT APPLICATION NUMBER: US/10/047,253
 C-> 13 <141> CURRENT FILING DATE: 2002-01-14
 13 <150> PRIOR APPLICATION NUMBER: US 60/261,314
 14 <151> PRIOR FILING DATE: 2001-01-12
 16 <150> PRIOR APPLICATION NUMBER: US 60/322,322
 17 <151> PRIOR FILING DATE: 2001-09-14
 19 <150> PRIOR APPLICATION NUMBER: US 60/322,030
 20 <151> PRIOR FILING DATE: 2001-09-14
 22 <160> NUMBER OF SEQ ID NOS: 22
 24 <170> SOFTWARE: PatentIn version 3.1
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 14
 28 <212> TYPE: PRT
 29 <213> ORGANISM: Artificial sequence
 31 <220> FEATURE:
 32 <223> OTHER INFORMATION: JAM domain
 34 <220> FEATURE:
 35 <221> NAME/KEY: MISC_FEATURE
 36 <222> LOCATION: (1)..(14)
 37 <223> OTHER INFORMATION: Xaa is any amino acid
 39 <400> SEQUENCE: 1
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 42 1 5 10
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 46 <211> LENGTH: 17
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 48 <213> ORGANISM: Artificial sequence
 50 <220> FEATURE:
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 53 <220> FEATURE:
 54 <221> NAME/KEY: MISC_FEATURE
 55 <222> LOCATION: (3)..(3)
 56 <223> OTHER INFORMATION: Xaa is Tyr or Ile
 58 <220> FEATURE:
 59 <221> NAME/KEY: MISC_FEATURE

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60 <222> LOCATION: (5)..(5)
61 <223> OTHER INFORMATION: Xaa is Ser or Thr
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64 <221> NAME/KEY: MISC_FEATURE
65 <222> LOCATION: (8)..(16)
66 <223> OTHER INFORMATION: Xaa is any amino acid
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71 1 5 10 15
74 Asp
78 <210> SEQ ID NO: 3
79 <211> LENGTH: 246
80 <212> TYPE: PRT
81 <213> ORGANISM: Homo sapiens
83 <400> SEQUENCE: 3
85 Thr Met Ile Ile Met Asp Ser Phe Ala Leu Pro Val Glu Gly Thr Glu 15
86 1 5 10 15
89 Thr Arg Val Asn Ala Gln Ala Ala Ala Tyr Glu Tyr Met Ala Ala Tyr 30
90 20 25 30
93 Ile Glu Asn Ala Lys Gln Val Gly Arg Leu Glu Asn Ala Ile Gly Trp 45
94 35 40 45
97 Tyr His Ser His Pro Gly Tyr Gly Cys Trp Leu Ser Gly Ile Asp Val 60
98 50 55 60
101 Ser Thr Gln Met Leu Asn Gln Gln Phe Gln Glu Pro Phe Val Ala Val 80
102 65 70 75
105 Val Ile Asp Pro Thr Arg Thr Ile Ser Ala Gly Lys Val Asn Leu Gly 95
106 85 90 95
109 Ala Phe Arg Thr Tyr Pro Lys Gly Tyr Lys Pro Pro Asp Glu Gly Pro 110
110 100 105 110
113 Ser Glu Tyr Gln Thr Ile Pro Leu Asn Lys Ile Glu Asp Phe Gly Val 125
114 115 120 125
117 His Cys Lys Gln Tyr Tyr Ala Leu Glu Val Ser Tyr Phe Lys Ser Ser 140
118 130 135 140
121 Leu Asp Arg Lys Leu Leu Glu Leu Leu Trp Asn Lys Tyr Trp Val Asn 160
122 145 150 155 160
125 Thr Leu Ser Ser Ser Leu Leu Thr Asn Ala Asp Tyr Thr Thr Gly 175
126 165 170 175
129 Gln Val Phe Asp Leu Ser Glu Lys Leu Glu Gln Ser Glu Ala Gln Leu 190
130 180 185
133 Gly Arg Gly Ser Phe Met Leu Gly Leu Glu Thr His Asp Arg Lys Ser 205
134 195 200 205
137 Glu Asp Lys Leu Ala Lys Ala Thr Arg Asp Ser Cys Lys Thr Thr Ile 220
138 210 215 220
141 Glu Ala Ile His Gly Leu Met Ser Gln Val Ile Lys Asp Lys Leu Phe 240
142 225 230 235 240
145 Asn Gln Ile Asn Ile Ser 245
146 245
149 <210> SEQ ID NO: 4
150 <211> LENGTH: 245

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244	65	70	75	80												
247	Gln	Gln	Cys	Ala	Val	Pro	Glu	Lys	Gln	Asp	Ile	Met	Lys	Lys	Leu	Lys
248															95	
251	Glu	Ile	Ala	Phe	Pro	Arg	Thr	Asp	Glu	Leu	Lys	Asn	Asp	Leu	Leu	Lys
252															110	
255	Lys	Tyr	Asn	Val	Glu	Tyr	Gln	Glu	Tyr	Leu	Gln	Ser	Lys	Asn	Lys	Tyr
256															125	
259	Lys	Ala	Glu	Ile	Leu	Lys	Lys	Leu	Glu	His	Gln	Arg	Leu	Ile	Glu	Ala
260															140	
263	Glu	Arg	Lys	Arg	Ile	Ala	Gln	Met	Arg	Gln	Gln	Gln	Leu	Glu	Ser	Glu
264															160	
267	Gln	Phe	Leu	Phe	Phe	Glu	Asp	Gln	Leu	Lys	Lys	Gln	Glu	Leu	Ala	Arg
268															175	
271	Gly	Gln	Met	Arg	Ser	Gln	Gln	Thr	Ser	Gly	Leu	Ser	Glu	Gln	Ile	Asp
272															190	
275	Gly	Ser	Ala	Leu	Ser	Cys	Phe	Ser	Thr	His	Gln	Asn	Asn	Ser	Leu	Leu
276															205	
279	Asn	Val	Phe	Ala	Asp	Gln	Pro	Asn	Lys	Ser	Asp	Ala	Thr	Asn	Tyr	Ala
280															220	
283	Ser	His	Ser	Pro	Pro	Val	Asn	Arg	Ala	Leu	Thr	Pro	Ala	Ala	Thr	Leu
284															240	
287	Ser	Ala	Val	Gln	Asn	Leu	Val	Val	Glu	Gly	Leu	Arg	Cys	Val	Val	Leu
288															255	
291	Pro	Glu	Asp	Leu	Cys	His	Lys	Phe	Leu	Gln	Leu	Ala	Glu	Ser	Asn	Thr
292															270	
295	val	Arg	Gly	Ile	Glu	Thr	Cys	Gly	Ile	Leu	Cys	Gly	Lys	Leu	Thr	His
296															285	
299	Asn	Glu	Phe	Thr	Ile	Thr	His	Val	Ile	Val	Pro	Lys	Gln	Ser	Ala	Gly
300															300	
303	Pro	Asp	Tyr	Cys	Asp	Met	Glu	Asn	Val	Glu	Glu	Leu	Phe	Asn	Val	Gln
304															320	
307	Asp	Gln	His	Asp	Leu	Leu	Thr	Leu	Gly	Trp	Ile	His	Thr	His	Pro	Thr
308															335	
311	Gln	Thr	Ala	Phe	Leu	Ser	Ser	Val	Asp	Leu	His	Thr	His	Cys	Ser	Tyr
312															350	
315	Gln	Leu	Met	Leu	Pro	Glu	Ala	Ile	Ala	Ile	Val	Cys	Ser	Pro	Lys	His
316															365	
319	Lys	Asp	Thr	Gly	Ile	Phe	Arg	Leu	Thr	Asn	Ala	Gly	Met	Leu	Glu	Val
320															380	
323	Ser	Ala	Cys	Lys	Lys	Lys	Gly	Phe	His	Pro	His	Thr	Lys	Glu	Pro	Arg
324															400	
327	Leu	Phe	Ser	Ile	Cys	Lys	His	Val	Leu	Val	Lys	Asp	Ile	Lys	Ile	Ile
328															415	
331	328	Val	Leu	Asp	Leu	Arg										
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336	<211>	LENGTH:	461													
337	<212>	TYPE:	PRT													
338	<213>	ORGANISM:	Homo sapiens													

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340 <400> SEQUENCE: 6
 342 Met Asp Gln Pro Phe Thr Val Asn Ser Leu Lys Lys Leu Ala Ala Met
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 344 Pro Asp His Thr Asp Val Ser Leu Ser Pro Glu Glu Arg Val Arg Ala
 345 20 25 30
 346 Leu Ser Lys Leu Gly Cys Asn Ile Thr Ile Ser Glu Asp Ile Thr Pro
 347 35 40 45
 348 50 55 60
 349 Arg Arg Tyr Phe Arg Ser Gly Val Glu Met Glu Arg Met Ala Ser Val
 350 70 75 80
 351 80 85 90 95
 352 95 100 105 110
 353 110 115 120 125
 354 Tyr Asn Val Glu Tyr Gln Glu Tyr Leu Gln Ser Lys Asn Lys Tyr Lys
 355 130 135 140 145
 356 150 155 160 165
 357 165 170 175 180
 358 Ala Glu Ile Leu Lys Lys Leu Glu His Gln Arg Leu Ile Glu Ala Glu
 359 180 185 190 195
 360 195 200 205 210
 361 210 215 220 225
 362 225 230 235 240
 363 240 245 250 255
 364 His Ser Pro Pro Val Asn Arg Ala Leu Thr Pro Ala Ala Thr Leu Ser
 365 255 260 265 270
 366 270 275 280 285
 367 285 290 295 300
 368 295 300 305 310
 369 310 315 320 325
 370 325 330 335 340
 371 340 345 350 355
 372 355 360 365 370
 373 370 375 380 385
 374 385 390 395 400

VERIFICATION SUMMARY
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L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:41 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:70 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2